



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/843221

Source: OIE

Date Processed by STIC: 08/28/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OIPE

RAW SEQUENCE LISTING

DATE: 08/28/2001

PATENT APPLICATION: US/09/843,221

TIME: 10:25:17

Input Set : A:\ES.txt

Output Set: N:\CRF3\08282001\I843221.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: KOSTENUIK, PAUL
 4 LIU, CHUAN-FA
 5 LACEY, DAVID LEE
 7 <120> TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
 PARATHYROID HORMONE-

Page 9 of 10A

8 RELATED PROTEIN
 10 <130> FILE REFERENCE: A-665B
 12 <140> CURRENT APPLICATION NUMBER: 09/843,221
 13 <141> CURRENT FILING DATE: 2001-04-26
 15 <150> PRIOR APPLICATION NUMBER: 60/266,673
 16 <151> PRIOR FILING DATE: 2001-02-06
 18 <150> PRIOR APPLICATION NUMBER: 60/214,860
 19 <151> PRIOR FILING DATE: 2000-06-28
 21 <150> PRIOR APPLICATION NUMBER: 60/200,053
 22 <151> PRIOR FILING DATE: 2000-04-27
 24 <160> NUMBER OF SEQ ID NOS: 170
 26 <170> SOFTWARE: PatentIn version 3.1
 28 <210> SEQ ID NO: 1
 29 <211> LENGTH: 684
 30 <212> TYPE: DNA
 31 <213> ORGANISM: Homo sapiens
 33 <220> FEATURE:
 34 <221> NAME/KEY: CDS
 35 <222> LOCATION: (1)..(684)
 36 <223> OTHER INFORMATION:
 39 <400> SEQUENCE: 1

40	atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg	48
41	Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu	
42	1 5 10 15	
44	ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc	96
45	Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu	
46	20 25 30	
48	atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc	144
49	Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser	
50	35 40 45	
52	cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag	192
53	His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu	
54	50 55 60	
56	gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg	240
57	Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr	
58	65 70 75 80	
60	tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat	288
61	Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn	
62	85 90 95	
64	ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc	336
65	Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro	
66	100 105 110	
68	atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag	384

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Input Set : A:\ES.txt

Output Set: N:\CRF3\08282001\I843221.raw

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69 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
70      115      120      125
72 gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc      432
73 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
74      130      135      140
76 agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg      480
77 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
78 145      150      155      160
80 gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct      528
81 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
82      165      170      175
84 ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc      576
85 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
86      180      185      190
88 gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg      624
89 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
90      195      200      205
92 atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg      672
93 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
94      210      215      220
96 tct ccg ggt aaa      684
97 Ser Pro Gly Lys
98 225
101 <210> SEQ ID NO: 2
102 <211> LENGTH: 228
103 <212> TYPE: PRT
104 <213> ORGANISM: Homo sapiens
106 <400> SEQUENCE: 2
108 Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
109 1      5      10      15
112 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
113      20      25      30
116 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
117      35      40      45
120 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
121      50      55      60
124 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
125 65      70      75      80
128 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
129      85      90      95
132 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
133      100      105      110
136 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
137      115      120      125
140 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
141      130      135      140
144 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145 145      150      155      160
148 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro

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149          165          170          175
152 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
153          180          185          190
156 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
157          195          200          205
160 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
161          210          215          220
164 Ser Pro Gly Lys
165 225
168 <210> SEQ ID NO: 3
169 <211> LENGTH: 21
170 <212> TYPE: PRT
171 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: PTH/PTHrP
176 <220> FEATURE:
177 <221> NAME/KEY: misc_feature
178 <222> LOCATION: (1)..(1)
179 <223> OTHER INFORMATION: Optional attachment to X3X4X5X6X7, X2X3X4X5X6X7,
X1X2X3X4X5X6X7
180      , or YX1X2X3X4X5X6X7
183 <220> FEATURE:
184 <221> NAME/KEY: misc_feature
185 <222> LOCATION: (1)..(1)
186 <223> OTHER INFORMATION: X8 is an amino acid residue (nonfunctional residue
preferred, M o
187      r Nle most preferred)
190 <220> FEATURE:
191 <221> NAME/KEY: misc_feature
192 <222> LOCATION: (3)..(3)
193 <223> OTHER INFORMATION: X10 is an amino acid residue (an acidic or hydrophilic
residue pr
194      eferred, N or D most preferred)
197 <220> FEATURE:
198 <221> NAME/KEY: misc_feature
199 <222> LOCATION: (4)..(4)
200 <223> OTHER INFORMATION: X11 is an amino acid residue (nonfunctional or basic residue
pref
201      erred, L, R, or K most preferred)
204 <220> FEATURE:
205 <221> NAME/KEY: misc_feature
206 <222> LOCATION: (5)..(5)
207 <223> OTHER INFORMATION: X12 is an amino acid residue (nonfunctional or aromatic
residue p
208      referred, G, F, or W most preferred)
211 <220> FEATURE:
212 <221> NAME/KEY: misc_feature
213 <222> LOCATION: (7)..(7)
214 <223> OTHER INFORMATION: X14 is an amino acid residue (basic or hydrophilic residue
prefer
215      red, H or S most preferred)
218 <220> FEATURE:
219 <221> NAME/KEY: misc_feature

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220 <222> LOCATION: (8)..(8)

221 <223> OTHER INFORMATION: X15 is an amino acid residue (nonfunctional residue preferred, wi

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222 th L or I most preferred)
 225 <220> FEATURE:
 226 <221> NAME/KEY: misc_feature
 227 <222> LOCATION: (9)..(9)
 228 <223> OTHER INFORMATION: X16 is an amino acid residue (nonfunctional or hydrophilic
 residu
 229 e preferred, Q, N, S, or A most preferred)
 232 <220> FEATURE:
 233 <221> NAME/KEY: misc_feature
 234 <222> LOCATION: (10)..(10)
 235 <223> OTHER INFORMATION: X17 is an amino acid residue (acidic, hydrophilic, or
 nonfunction
 236 al residue preferred, S, D, or L most preferred)
 239 <220> FEATURE:
 240 <221> NAME/KEY: misc_feature
 241 <222> LOCATION: (11)..(11)
 242 <223> OTHER INFORMATION: X18 is an amino acid residue (nonfunctional residue
 preferred,M,
 243 L, V or Nle most preferred)
 246 <220> FEATURE:
 247 <221> NAME/KEY: misc_feature
 248 <222> LOCATION: (12)..(12)
 249 <223> OTHER INFORMATION: X19 is an amino acid residue (acidic or basic residue
 preferred,
 250 E or R most preferred)
 253 <220> FEATURE:
 254 <221> NAME/KEY: misc_feature
 255 <222> LOCATION: (14)..(14)
 256 <223> OTHER INFORMATION: X21 is an amino acid residue (nonfunctional residue or basic
 res
 257 idue preferred; V, M, R, or Nle most preferred)
 260 <220> FEATURE:
 261 <221> NAME/KEY: misc_feature
 262 <222> LOCATION: (15)..(15)
 263 <223> OTHER INFORMATION: X22 is an amino acid residue (hydrophilic, acidic, or
 aromatic r
 264 esidue preferred, E or F most preferred)
 267 <220> FEATURE:
 268 <221> NAME/KEY: misc_feature
 269 <222> LOCATION: (16)..(16)
 270 <223> OTHER INFORMATION: X23 is an aromatic or lipophilic residue (W or F preferred)
 273 <220> FEATURE:
 274 <221> NAME/KEY: misc_feature
 275 <222> LOCATION: (17)..(17)
 276 <223> OTHER INFORMATION: X24 is a lipophilic residue (L preferred)
 279 <220> FEATURE:
 280 <221> NAME/KEY: misc_feature
 281 <222> LOCATION: (18)..(18)
 282 <223> OTHER INFORMATION: X25 is an amino acid residue (hydrophilic or basic residue
 prefe
 283 rred, R or H most preferred)
 286 <220> FEATURE:
 287 <221> NAME/KEY: misc_feature

288 <222> LOCATION: (19)..(19)
289 <223> OTHER INFORMATION: X26 is an amino acid residue (hydrophilic or basic residue
prefe
290 rred, K or H most preferred)

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293 <220> FEATURE:
 294 <221> NAME/KEY: misc_feature
 295 <222> LOCATION: (20)..(20)
 296 <223> OTHER INFORMATION: X27 is an amino acid residue (lipophilic, basic, or nonfunctional)
 297 1 residue preferred, K or L most preferred)
 300 <220> FEATURE:
 301 <221> NAME/KEY: misc_feature
 302 <222> LOCATION: (21)..(21)
 303 <223> OTHER INFORMATION: X28 is an amino acid residue (lipophilic or nonfunctional residue)
 304 e preferred, L or I most preferred)
 307 <220> FEATURE:
 308 <221> NAME/KEY: misc_feature
 309 <222> LOCATION: (21)..(21)
 310 <223> OTHER INFORMATION: Optional attachment to X29, X29X30, X29X30X31, X29X30X31X32, X29
 311 X30X31X32X33, X29X30X31X32X33X34, X29X30X31X32X33X34X35, or X29X
 312 30X31X32X33X34X35X36
 315 <400> SEQUENCE: 3
 W--> 317 Xaa His Xaa Xaa Xaa Lys Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa Xaa
 318 1 5 10 15
 W--> 321 Xaa Xaa Xaa Xaa Xaa
 322 20
 325 <210> SEQ ID NO: 4
 326 <211> LENGTH: 22
 327 <212> TYPE: PRT
 328 <213> ORGANISM: Artificial Sequence
 330 <220> FEATURE:
 331 <223> OTHER INFORMATION: PTH/PTHrP
 333 <220> FEATURE:
 334 <221> NAME/KEY: misc_feature
 335 <222> LOCATION: (1)..(1)
 336 <223> OTHER INFORMATION: Optional attachment to J1J2J3J4J5J6, J2J3J4J5J6, J3J4J5J6
 339 <220> FEATURE:
 340 <221> NAME/KEY: misc_feature
 341 <222> LOCATION: (1)..(1)
 342 <223> OTHER INFORMATION: J7 is an amino acid residue (nonfunctional or aromatic residue)
 343 eferred, L or F most preferred)
 346 <220> FEATURE:
 347 <221> NAME/KEY: misc_feature
 348 <222> LOCATION: (2)..(2)
 349 <223> OTHER INFORMATION: J8 is an amino acid residue (nonfunctional residue preferred, M o
 350 r Nle most preferred)
 353 <220> FEATURE:
 354 <221> NAME/KEY: misc_feature
 355 <222> LOCATION: (6)..(6)
 356 <223> OTHER INFORMATION: J12 is an amino acid residue (nonfunctional or aromatic residue)
 357 referred, G or W most preferred)
 360 <220> FEATURE:

361 <221> NAME/KEY: misc_feature
362 <222> LOCATION: (10)..(10)

Asn Phe

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/843,221

DATE: 08/28/2001

TIME: 10:25:18

Input Set : A:\ES.txt

Output Set: N:\CRF3\08282001\I843221.raw

L:317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:321 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:396 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:471 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:703 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:705 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:705 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: *Erased*